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My research focuses on childhood immune and allergy development in relation to maternal immunity and microbial exposure. I am an immunologist collaborating with paediatric allergologists, obstetricians, clinical immunologists and microbiologists. Our research is translational, combining advanced laboratory methodology with careful, long-term, clinical follow-up during pregnancy and childhood with excellent compliance rates, also in randomised placebo-controlled intervention studies (see e.g. ClinicalTrials.gov Identifier NCT01542970). In my laboratory at the Division of Inflammation Medicine at Linköping University, Sweden, we analyse systemic and mucosal immune function by ELISA, Luminex, flow cytometry, real time PCR and EIA (epigenetic immune lineage analysis).

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stimulation, resulting in an abnormal postnatal immune maturation. The gut microbiota is quantitatively the most important source of microbial stimulation and may provide a primary signal for appropriate immune development. While no specific microbes with consistently harmful or allergy protective roles have yet been identified, the gut microbiota differs in composition and diversity during the first months of life in children who later do or do not develop allergic disease. Early establishment of a diverse gut microbiota may be more important than the distribution of specific microbial species in shaping a normal immune maturation. It is also becoming increasingly evident that the maternal microbial environment during pregnancy is important in childhood immune programming. A combined pre- and postnatal supplementation seems to be crucial for the preventive effect of probiotics on infant eczema. Probiotic interventions have so far failed to prevent asthma, however. Further studies on the appropriate timing of interventions and the complex interactions between the infant immune system and the gut microbiota are required to identify preventive strategies to combat the asthma and allergy epidemic.



Kieran Tuohy

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KIERAN TUOHY received his PhD from the University of Surrey (UK) in 2000. Between 2000 and 2006 he worked as a post doctoral researcher in the Food Microbial Sciences Unit of Professor Glenn Gibson, University of Reading and in 2006, was appointed lecturer in the Department of Food Science and Nutrition, University of Reading. He now leads the Nutrition and Nutrigenomics Group at Fondazione Edmund Mach, Trento, Italy (<http://cri.fmach.eu/Research/Food-Quality-and-Nutrition/Nutrition-and-Nutrigenomics>) which grew out of the Autonomous Province of Trento funded incoming team project TrentinoGUT. His research focuses on the health effects of diet:microbe interactions within the gastrointestinal tract and has expertise in microbial ecology, fermentation technologies, nutrition, functional food design and testing, metabolomics and metagenomics. He has over 79 international, peer reviewed publications in the area of gut microbiology, a H index of 22, and is co-editor of the book "Diet-Microbe Interactions in the Gut", Elsevier.

Diet : Microbe interactions - ecosystem support

Recent metagenomic studies are confirming what pioneers in gut microbiology have long said, that diet:microbe interactions in the gut impact on human health and disease. The gut microbiota appear to regulate various physiological functions including host energy metabolism, immune homeostasis, and brain development and function. The gut microbiota produces a range of biologically active metabolites, not least, short chain fatty acids, small phenolic compounds derived from polyphenol metabolism, and, immunologically and neurologically active amino acid derivatives such as gamma-aminobutyric acid, serotonin and dopamine. Microbiota activities also control systemic tryptophan metabolism and peripheral concentrations of potentially harmful metabolites derived from choline and carnitine metabolism, notably the cardiotoxicant trimethylamine-N-oxide. The gut microbiota also determines the profile of bile acids returning to the liver through the enterohepatic circulation, important cell signalling molecules involved in various physiological functions, including host energy metabolism and immune function. Diet in large part regulates these important microbiota physiological services and dietary constituents, particularly the relative proportions of fermentable fiber and plant polyphenols on the one hand, and refined sugars, fat and animal protein, on the other, appear to critically determine the flux of either beneficial or potentially harmful metabolites from the gut. This presentation will discuss how diet regulates both the composition and metabolic output of the gut microbiota constituting, in effect, ecosystem support, not just for the gut microbiota, but for the greater human:microbe ecosystem as a whole.